

E. O'Hara

#6

1646

RAW SEQUENCE LISTING

DATE: 02/12/2001

PATENT APPLICATION: US/09/380,276

TIME: 16:36:59

Input Set : A:\ES.txt

Output Set: N:\CRF3\02122001\I380276.raw

P.S

ENTERED

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3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
5 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and utility of the
6   Polypeptides
8 <130> FILE REFERENCE: Q55589
10 <140> CURRENT APPLICATION NUMBER: 09/380,276
11 <141> CURRENT FILING DATE: 1999-08-27
13 <150> PRIOR APPLICATION NUMBER: JP 9-43143
14 <151> PRIOR FILING DATE: 1997-02-27
16 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799
17 <151> PRIOR FILING DATE: 1997-02-27
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1269
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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33 gatcgggtctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag      180
35 gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggtt      240
37 aaggaggact ggggcttcca gaaatgcaag ccctgtcttg actgcgcagt ggtgaaccgc      300
39 tttcagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga      360
41 ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac      420
43 cctcctcctc cttacgaacc gcaactgtgc agcaaggtea acctcgtgaa gatcgcgtcc      480
45 acggcctcca gcccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc      540
47 gtctgtctgg cctgtctcat cctctgtgtc atctattgta agagacagtt tatggagaag      600
49 aaacccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt      660
51 cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac      720
53 tcagtgcaga cctgcggggc ggtgcgcttg ctcccatcca tgtgtgtgta ggaggcctgc      780
55 agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga      840
57 aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc      900
59 tgtggcgagt tttcagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc      960
61 tctttttgtg actcttatcc tgaactcact ggagaagaca ttcattctct caatccagaa      1020
63 cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctgtt      1080
65 ccagtccagt ctcatctgta aaactttaca gcagctactg atttatctag atataacaac      1140
67 aacttgtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag      1200
69 gagagtggcg ctatcatcca cccagccact cagacgtccc tccaggtaag gcagcgactg      1260
71 ggttccctg                                     1269

74 <210> SEQ ID NO: 2
75 <211> LENGTH: 1704
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 2
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82 tactagaaca agagaaaacg tttttcactc ttttagtatt actaggctat ttgtcatgta      120
84 aagtgacttg tgaacacagga gactgtagac agcaagaatt cagggatcgg tctggaaact      180

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86 gtgttccctg caaccagtgt gggccaggca tggagttgtc taaggaaatgt ggcttcggct 240
88 atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct 300
90 tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt 360
92 gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga 420
94 aacttgctgg ctttcaagac atggagtgtg tgccttggtg agaccctcct cctccttacg 480
96 aaccgcactg tgccagcaag gtcaacctcg tgaagatcgc gtccacggcc tccagccac 540
98 gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc 600
100 tcctcctctg tgtcatctat tgtaagagac agtttatgga gaagaaaccc agctggtctc 660
102 tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc 720
104 tccacgaata tgcccacaga gcctgctgcc agtgccgccc tgactcagtg cagacctgcg 780
106 ggccgggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aaccggcgga 840
108 ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg 900
110 gggagatggg gccgactttc ttccgatccc tcacgcagtc catctgtggc gaggtttcag 960
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114 atcctgaact cactggagaa gacattcatt ctctcaatcc agaactgaa agctcaacgt 1080
116 ctttggaattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt 1140
118 ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag 1200
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122 tccaccagc cactcagacg tccctccagg aagcttaaaag aacctgcttc tttctgcagt 1320
124 agaagcgtgt gctggaaccc aaagagtact cctttgttag gcttatggac tgagcagtct 1380
126 ggaccttgca tggcttctgg ggcaaaaata aatctgaacc aaactgacgg catttgaagc 1440
128 ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa 1500
130 gaaaagactc caggccgact catgatactc tgcactcttc ctacatgaga agcttctctg 1560
132 ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat 1620
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145 <221> NAME/KEY: misc_feature
146 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (45)..(1295)
153 <220> FEATURE:
154 <221> NAME/KEY: sig_peptide
155 <222> LOCATION: (45)..(119)
157 <220> FEATURE:
158 <221> NAME/KEY: mat_peptide
159 <222> LOCATION: (120)..()
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162 gggaaacgtag aactctccaa caataaatac atttgataag aaag atg gct tta aaa 56
163 Met Ala Leu Lys
164 -25
166 gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta 104
167 Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu
168 -20 -15 -10

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170	ggc	tat	ttg	tca	tgt	aaa	gtg	act	tgt	gaa	aca	gga	gac	tgt	aga	cag	152
171	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Thr	Gly	Asp	Cys	Arg	Gln	
172	-5				-1	1				5					10		
174	caa	gaa	ttc	agg	gat	cgg	tct	gga	aac	tgt	gtt	ccc	tgc	aac	cag	tgt	200
175	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro	Cys	Asn	Gln	Cys	
176				15					20					25			
178	ggg	cca	ggc	atg	gag	ttg	tct	aag	gaa	tgt	ggc	ttc	ggc	tat	ggg	gag	248
179	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly	Tyr	Gly	Glu	
180			30					35					40				
182	gat	gca	cag	tgt	gtg	acg	tgc	cgg	ctg	cac	agg	ttc	aag	gag	gac	tgg	296
183	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	Lys	Glu	Asp	Trp	
184		45					50					55					
186	ggc	ttc	cag	aaa	tgc	aag	ccc	tgt	ctg	gac	tgc	gca	gtg	gtg	aac	cgc	344
187	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	Val	Val	Asn	Arg	
188	60					65				70					75		
190	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	atc	tgc	ggg	gac	392
191	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	Ile	Cys	Gly	Asp	
192				80						85					90		
194	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	ggc	ttt	caa	gac	440
195	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	Gly	Phe	Gln	Asp	
196			95						100					105			
198	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	tac	gaa	ccg	cac	488
199	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	Tyr	Glu	Pro	His	
200			110					115					120				
202	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	acg	gcc	tcc	agc	536
203	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	Thr	Ala	Ser	Ser	
204		125					130					135					
206	cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	gct	ctg	gcc	acc	584
207	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	Ala	Leu	Ala	Thr	
208	140					145					150				155		
210	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	tgt	aag	aga	cag	632
211	Val	Leu	Leu	Ala	Leu	Ile	Leu	Cys	Val	Ile	Tyr	Cys	Lys	Arg	Gln		
212				160						165					170		
214	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	cag	gac	att	cag	680
215	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	Gln	Asp	Ile	Gln	
216				175						180				185			
218	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ctt	gac	aga	cct	cag	ctc	cac	gaa	728
219	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	Gln	Leu	His	Glu	
220			190					195					200				
222	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	tca	gtg	cag	acc	776
223	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	Ser	Val	Gln	Thr	
224		205					210					215					
226	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	gag	gag	gcc	tgc	824
227	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	Glu	Glu	Ala	Cys	
228	220					225						230				235	
230	agc	ccc	aac	ccg	gcg	act	ctt	ggt	tgt	ggg	gtg	cat	tct	gca	gcc	agt	872
231	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	Ser	Ala	Ala	Ser	
232				240							245				250		
234	ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	gtg	ccg	act	ttc	920

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236          255          260          265
238 ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg      968
239 Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp
240          270          275          280
242 cct ctg atg cag aat ccc atg ggt gac aac atc tct ttt tgt gac      1016
243 Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
244          285          290          295
246 tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa      1064
247 Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
248 300          305          310          315
250 ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt      1112
251 Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
252          320          325          330
254 ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct      1160
255 Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
256          335          340          345
258 act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act      1208
259 Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
260          350          355          360
262 cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct      1256
263 Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
264          365          370          375
266 atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct      1305
267 Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
268 380          385          390
270 gcttcttttct gcagtagaag cgtgtgctgg aacccaaaga gtactccttt gttaggctta      1365
272 tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact      1425
274 gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac      1485
276 ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttctaca      1545
278 tgagaagcct ctctgccaca aaagtgactt caaagacgga tgggttgagc tggcagccta      1605
280 tgagattgtg gacatataac aagaaacaga aatgccctca tgcttatatt catggtgatt      1665
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286 <211> LENGTH: 417
287 <212> TYPE: PRT
288 <213> ORGANISM: Homo sapiens
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291 <221> NAME/KEY: misc_feature
292 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
294 <400> SEQUENCE: 4
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301          -5          -1 1          5
304 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
305          10          15          20
308 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
309          25          30          35

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312 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
313 40 45 50 55
316 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
317 60 65 70
320 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
321 75 80 85
324 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
325 90 95 100
328 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
329 105 110 115
332 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
333 120 125 130 135
336 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
337 140 145 150
340 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
341 155 160 165
344 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
345 170 175 180
348 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
349 185 190 195
352 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
353 200 205 210 215
356 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
357 220 225 230
360 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
361 235 240 245
364 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
365 250 255 260
368 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
369 265 270 275
372 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
373 280 285 290 295
376 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
377 300 305 310
380 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
381 315 320 325
384 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
385 330 335 340
388 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
389 345 350 355
392 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
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396 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
397 380 385 390
400 Ala
404 <210> SEQ ID NO: 5
405 <211> LENGTH: 1269
406 <212> TYPE: DNA
407 <213> ORGANISM: Homo sapiens

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/380,276

DATE: 02/12/2001
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Input Set : A:\ES.txt
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L:787 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:787 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9